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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB E Maximum DB E

Database

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 840367
R;Kiein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
A;Reterence number: 840312; MUID:94080891; PMID:8258341
A;Residues: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-127 <KLE>
A;Cross-references: EMEL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S40331
R;Klein, R; Jaenichen, R; Zachau, H.G.
Eur. J. Immunol: 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MuID: 94080891; PMID: 8258341
A;Accession: S40331
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 «KLE>
A;Cross-references: EMBL: X72441; NID: 9441350; PIDN: CAA51109.1; PID: 9441351
C;Reywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology < IMM>
Ig kappa chain - h
Ig kappa chain V-J
Ig kappa chain V-I
Ig kappa chain V-I
Ig kappa chain V
Ig kappa chain V
Ig kappa chain V
Ig kappa chain - h
Ig Ight chain var
Ig kappa chain - h
Ig kappa chain - h
Ig kappa chain - h
Ig kappa chain V-J
Ig kappa chain V-J
Ig kappa chain V-J
Ig kappa chain V-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 DIOMTOSPSSLSASVGDRVTITCRASQSI----SNYLNWYQRKPGKAPKCLIYAASSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 GVPSRFSGSGSGTDFTLTISSLQPEDFATYCQQSYNIPWTFGQGTKVEIKRTV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.6%; Score 498; DB 2; Length 12 ilarity 85.1%; Pred. No. 1.3e-36; Conservative 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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                     S40349
KIHUOU
S340368
S360375
JL0139
S32001
S31983
S46376
S46376
KIHULN
KIHULN
S52789
                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V-J-C region - human
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Matches
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1545.812 Million cell updates/sec
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1 DIQLTQSPSSLSASVGDRVT.....SHEDPYTFGQGTKVEIKRTV 114
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                                                                                                                              3, 2005, 08:53:28 ; Search time 7.09576 Seconds
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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K1HUDE
S40369
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S40370
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Gapop 10.0 , Gapext 0.5
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S40314
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S40317
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S31979
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seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*
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469 468 465.5

Score

Result No.

459 458 457 457 457

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Gaps

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Ig kappa chain V-J region (T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46370; S38644, P.; Zouali, M.
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene reash A;Reference number: S46369; MuID:94313975; PMID:8039491
                                                                                                                                                                                                                                                                                                                 A; Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re A; Reference number: $44105
A; Accession: $44122
                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: 84412
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
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Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Cross-references: EMBL:227171; NID:g415957; PIDN:CAA81695.1; PID:g415958 C, Superfamily: immunoglobulin V region; immunoglobulin homology C, Reywords: heterotetramer; immunoglobulin E; E, Reywords: heterotetramer; immunoglobulin F; 26-100/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 DIQMTQSPSSLSASVGDRVTITCRASRSI----SSFLNWYQQKPGKAPQLLIYAVSRLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z31390; NID:g472976; PIDN:CAAB3265.1; PID:g940533 C;Superfamily: immunoglobulin V reggion; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin Pilo:g910753789.076979 immunoglobulin homology  F;16-90/Domain: immunoglobulin homology 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDP--YTFGQGTKVEIKR 112
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No. 3.4e-34; Indels
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Pred. No. 2.5e-34;
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Local Similarity 81.6%;
nes 93; Conservative
                                                                                                                                                             Ig kappa chain V region - human
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                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <HAW>
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A; Residues: 1-120 <BEN>
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                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes A;Reference number: A49047; MUID:92387224; PMID:1516616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. Accession: 3.1998
R. Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
A. Description: Lack of promiscuity in autoantigen-specific H and L chain combinations
A. Reference number: S31977
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C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                                                                                 17 DIQMTQSPSSLSASVGDRVTITCRASQSI----SSYLNWYQQKPGKAPKLLIYAASSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIQMTQSPSSLSASVGDRVTITCRASQSI----SSYLNWYQQKPGKAPKLLIYAASSLQS
                                                                               1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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                              Indels
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     Pred. No. 1.2e-35;
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     86.58;
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                           96; Conservative
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A;Molecule type: nucleic acid
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Matches 91; Conserv
  Best Local Similarity
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A, Note: the C region of this chain has the Inv (3) marker R; Steiner, V.; Chang, J.Y.
FRBS Lett. 222, 6-10, 1987
A, Title: Chemical modification of the carboxyl groups of protein substrates enhances their A, Reference number: S02572; MUID: 88005152; PMID: 3115831
A, Contents: annotation
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C; Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapp
C; Complex: an immunoglobulin heterotetramer; such as IgA and IgM, the subunits associate into lan
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
E; 16-90/Domain: immunoglobulin homology <IMM>
F; 16-90/Domain: immunoglobulin pomology <IMM>
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C'Species: Homo sapiens (man)
C'Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C'Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C'Accession: A. Hilschman, N.
Hoppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970
A,Title: The primary structure of a monoclonal kappa-type immunoglobulin L-(A,Reference number: A01868; MUID:71032830; PMID:4097974
A,Reference number: A01868; MUID:71032830; PMID:4097974
                                                                                                                                                                                                                                                              16 DIQMTQSPSSLSASVGDRVTFTCRSSQTI----GTYLNWYQQKPGQAPKLLIFAASSLLN
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           immunoglobulin homology
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                                                                                                                     ; Score 465.5; DB 2;
; Pred. No. 8.8e-34;
11; Mismatches 7;
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81.2%; Pred. No. 1e-33;
iive 10; Mismatches 7;
           C;Superfamily: immunoglobulin V region; immunoc
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-108 <WAT>
A;Cross-references: UNIPROT:P01600
                                                                                                                                               79.88;
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R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: S47181
A;Accession: S47182
A;Accession: S71182
A;Accession: preliminary
A;Accession: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 cMCI>
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R; Portcolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
A; Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as A; Reference number: S31977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig Kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLAWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                         A;Cross-references: EMBL:X79786; NID:g506422; PIDN:CAA56182.1; PID:g506423 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 109;
4.6e-34;
thes 9; Indels
                                                                                                                                                                                                                                                                                                                                                                        Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
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                                                                                                                                                                                                                                                                                                                                                                  78.7%; Score 469; DB 2;
82.1%; Pred. No. 3.8e-34;
ive 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.5%; Score 468; DB 79.6%; Pred. No. 4.6e; ive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin v region; immunoc;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translation not shown
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.15
Marches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-109 < POR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S31981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
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Best Local (
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A; Molecule type: mRNA

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                                                                                                                                                                                                                                                                                                                  26
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C;Spate: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                             1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                           1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                   A;Cross-references: EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID:g1335386 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:X72480; NID:9441428; PIDN:CAA51148.1; PID:9441429; Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S40370
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40370
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3346-3271, 199
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
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                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                   61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR 112
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                                                                                                                                                    77.5%; Score 462; DB 2; Length 108; 81.2%; Pred. No. 1.5e-33;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                         9; Mismatches
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C; Keywords: heterotetramer; immunoglobusta.
F; 30-104/Domain: immunoglobulin homology <IMM>
                                                                                                F;16-90/Domain: immunoglobulin homology <IMM>
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A;Status: preliminary; translation not shown
A;Molecule type: mRNA
                                                                                                                                                                             Local Similarity 81.2:
les 91; Conservative
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Best Local Similarity
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les 92; Conserv
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A;Residues: 1-108 <MAR>
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                                                                                                                                                       Query Match
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Matches
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Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S52792
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the RMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-charactering number: S52789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CjAccession: $52793
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-& A;Reference number: $52793
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                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DIQMTQSPSSLSASVGDRVTITCRASQNI----ISYLNWYQQKPGKAPKLLMYAASSLQS
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                                                                                          22 DIQLIQSPSFLSASIGDRVTITCRASQGI----NSYLAWYQQKPGKAPKLLIYVASTLQS
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                                                      1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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C;Superfamily: immunoglobulin V reggion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/bomain: immunoglobulin homology <IMM>
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4; Gaps
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                                                                                                                                                                                                              78 GVPSRFSGSGSGTEFTLTISSLQPEDFASYYCQQFNSYPFTFGGGTKVEIRRTV 131
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9; Indels
Mismatches
10;
91; Conservative
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A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
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A; Residues: 1-129 <ROC>
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S52792
Matches
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Search completed: June 3, 2005, 09:17:50 Job time: 8.09576 secs

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3, 2005, 08:31:37; Search time 32.7497 Seconds (without alignments) 1782.523 Million cell updates/sec OM protein - protein search, using sw model June Run on:

US-10-791-619-8 596 1 DIQLTQSPSSLSASVGDRVTSHEDPYTFGQGTKVEIKRTV 114 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien		sapien	sapien			sapien	musculu	sapien	sapien	sapien	sapien	sapien	sapien	sapien	musculu	sapien	musculu		sapien	musculu
tion	homo	рошо	рошо	homo	homo	homo	homo	рошо	рошо	ношо	homo	homo	homo	homo	homo	рошо	рошо	พนธ ก	homo	homo	homo	homo	homo	homo	homo	แนยก	homo	เลก	homo	homod	mus n
Description	Q6gmx8	Q9u177	Q6gmw1	Q968a9	Qegmx0	Q6pih7	P01600	P01597	P04431	P01606	Q7z3y4	P01594	P04430	Q9u181	P01605	Q9u170	Q7z473	P01665	P01603	P01607	P01611	06gmx9	P01598	P01599	P80362	P01667	P01608	P01666	Q6pit5	P01610	P01664
	Q6GMX8	Q9UL77	QGGMW1	Q96SA9	Degmin 0	O6PIH7	KV1H HUMAN	KV1E HUMAN	KV1W HUMAN	KV1N HUMAN	Q7Z3 <u>Y</u> 4	KV1B HUMAN	KV1V HUMAN	9UL81	KV1M HUMAN	09UL70	Q7Z473	KV3M MOUSE	KV1K HUMAN	KV10 HUMAN	KV1S_HUMAN	5GMX9	KV1F HUMAN	KV1G HUMAN	KV1Y HUMAN	KV3O MOUSE	KV1P HUMAN	KV3N MOUSE	26PITS	KV1R HUMAN	KV3L_MOUSE
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% Query Match Length DB	80.7	80.5	78.9	78.6	78.2	78.0	77.9	76.5	76.0	75.5	74.8	74.7	74.7	74.4	74.3	74.2	74.2	74.0	73.8	73.8	73.5	73.3	73.2	73.2	73.2	73.2	72.8	72.8	72.8	72.7	72.7
Score	481	480	470	468.5	466	465	464	456	453	450	446	445	445	443.5	443	442	442	441	440	440	438	437	436	436	436	436	434	434	434	433	433
Result No.	-	7	m	4	S	9	7	80	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

	P01604 homo sapien Q6pih4 homo sapien									
KV3Q MOUSE Q9UL79	KV1L HUMAN O6PIH4	Q96PF6 Q65ZC8	KV1A HUMAN	KV1D HUMAN	KV1T HUMAN	KV3H MOUSE	<u>0652</u> 29	KV1Q HUMAN	<u>0811</u> <u>0</u> 6	KV1C_HUMAN
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111	108	116 244	108	101	109	111	240	108	111	108
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
  NCBI_TaxID=9606;
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                                                                                         1 DIQMIQSPSSLSASVGDRVTITCRASQSI----SSYLAWYQQKPGKAPNLLIYAASSLQS
                                                                           1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                        4; Gaps
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                                                                                                                     GVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
WL X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 80.5%; Score 480; DB 2; Length 108; 1 Similarity 83.9%; Pred. No. 3.3e-40; 94; Conservative 7; Mismatches 7; Indels
                                Length 236;
                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                          80.7%; Score 481; DB 2; Lengua 23.82.5%; Pred. No. 6.3e-40; wismarches 7; Indels
Hypothetical protein.
SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                    108 AA.
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INTERPO5, IPRO07110; IG-like.
INTERPO5, IPRO03596; IG-V.
SMART; SMO0406; IGV; I.
PROSITE; PS50835; IG-LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF035037; AAD56273.1;
PIR; B49047; B49047.
PIR; S34083; S34083.
                                                     94; Conservative
                                                                                                                                                                                                   PRELIMINARY;
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                                            Best Local Similarity
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A Straubberg R.L., Feingold E.A., Grouse L.H., Oberge J.G.,
RA Altschul S.P., Zeeberg B.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Jordan H., More T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.M., Dickson M.C.,
A Godriguez A.C., Grimwood J., Myres R.M., Butterfield Y.S.,
M. Jones S.J., Marra M.A.,
B. Mones S.J., Marra M.A.,
B. Mones S.J., Marra M.A.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
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01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptcoccal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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SEQUENCE 236 Aa; 25751 MW; 5BFE6A087AFAC437 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Query Match
Best Local Similarity bv..
Best Conservative
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SEQUENCE FROM N.A.
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Nausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Butchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broak S.A., McKernan K.J., Masley J.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachy J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Johes S.J., M
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                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPSRFSGSGSGTDFTLIISSLQPEDFATYYCQQSY-STLIFGGGTKVEIKR 107
              MEDLINE=98375893; PubMed=9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Molecular analysis of polyreactive monoclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes.";
J. Immunol. 161:2020-2031 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                       78.6%; Score 468.5; DB 2; Length 107; 84.8%; Pred. No. 4.6e-39; tive 5; Mismatches 7; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                     107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                   PIR, PHO867, PHO867.

PIR, S16840; S16840.

PIR, S34083; S34083.

PIR, S34086; S34086.

HSSP; PO1607; 1BWW.

INCEPPO; IPR007310; IG-like.

INCEPPO; IPR0073596; IG-v.

SWART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                      U96396; AAB68785.1; -
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.00
Best Local Similarity 84.84
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                    107
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Homo sapiens (Human).
                                                                                                                                          B49047; B49047
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EMBL; 1
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 DIQMTQSPSSLSASVGDRVTITCRASQNI----NNYLNWYQLKPGKAPNLLIYAASSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPSRFSGSGSGTDFTLTISSLRPDDFATYYCQQSYNIPLTFGGGTNVEIKRTV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausborger...

L Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

E EMBL; ECO73775, AAH13775.1; -..

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR00306; Ig-MHC.

R InterPro; IPR00306; Ig-WHC.

R InterPro; IPR00306; Ig-V.

R Pfam; PF007654; Cl.set; l.

R Pfam; PF007654; Cl.set; l.

R SWART; SW00407; IG. 2.

DR SWART; SW00407; IG. 2.

DR SWART; SW00406; IG. 2.

R PROSITE; PS50835; IG LIKE; 2.

DR PROSITE; PS50835; IG LIKE; 2.

DR PROSITE; PS50835; IG LIKE; 2.

R HYPOThetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 236;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                              78.2%; Score 466; DB 2;
80.7%; Pred. No. 2e-38;
iive 9; Mismatches
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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ID KV1W HUMAN
AC P04431;
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P01597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).

-!- MISCELLANBOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANBOUS: This is a Bence-Jones protein.
-!- MISCELLANBOUS: Th
                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe S., Hilschmann N.; "The primary structure of a monoclonal kappa-type immunoglobulin I chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                Length 236;
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Framework-2.
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           EMBL; BC034141, AAR3141.1; -. BMBL; BC03416, AR2141.1; -. BMBL; BC03416, AR3141.1; -. BMBL; BC0359; Ig.-ci.
InterPro; IPR00359; Ig.-ci.
InterPro; IPR003596; Ig.-v.
InterPro; IPR003596; Ig.-v.
InterPro; IPR003596; Ig.-v.
InterPro; IPR00406; Ig., I. SWART; SW00407; IG.2.
SWART; SW00406; IG.; I. SWART; SW00409; IG. LIKE; 2.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS50835; IG_MHC; UNKNOWN_1.
HYPOCHECICAL Droctein.
SEQUENCE 236 AA; 25603 MW; BBC561106861213F CRC64;
 (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                              78.0%; Score 465; DB 2;
82.5%; Pred. No. 2.5e-38;
tive 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
RAPPa chain V-I region Hau.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 82.55
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Milstein C.P., Deverson E.V.;
"The amino acid sequence of a human kappa light chain.";
Biochem. J. 123:945-958[1971].
Biochem. J. MSCELLANEOUS: The C region of this chain has the INV (3) marker.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                 61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 456; DB 1; Length 108;
; Pred. No. 8.2e-38;
10; Mismatches 10; Indels
                                                Length 108;
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                                                                                               7; Indels
108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;
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                                           Match 77.9%; Score 464; DB 1; Local Similarity 81.2%; Pred. No. 1.3e-38; les 91; Conservative 10; Mismatches 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Last sequence update), Last annotation update)
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HSSP, PO1607; 1BWW.
GO; GO:000576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SWART; SW00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
DOWAIN
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21-JUL-1986 (Rel. 01, Last seq
05-JUL-2004 (Rel. 44, Last ann
1g kappa chain V-I region DEE.
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78.6%;
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Similarity
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  NCBI_TaxID=9606;
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Matches
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SO STATE TEST TO SERVICE SO STATE SO SERVICE SO SERVICE
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                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 DIQMTQSPSSLSASVGDRVTITCRASQSI----SNYLNWYQQKPGKAPKLLIYAASSLQS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
                                                                                                                                                                                                                        MEDLINE=85014148; PubMed=6091049; Klobeck H.G., Combriato G., Zachau H.G.; Immunoglobulin genes of the Kappa light chain type from two human lymphoid cell lines are closely related."; Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%; Score 453; DB 1; Length 129; llarity 81.1%; Pred. No. 2e-37; Conservative 8; Mismatches 9; Indels
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                     13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Walker precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
RAppa chain V-I region OU.
Homo sapiens (Human).
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HSSP; P01607; 1BWW.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X00965; CAA25477.1; ALT_TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00406; ĬĠv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
(Rel. 05, Created)
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                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=9606;
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90;
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SEQUENCE
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SEQUENCE FROM N.A.

TISSUB-SKeletal Muscle;
TISSUB-SKeletal Muscle;
TISSUB-SKeletal Muscle;
A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Erownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boossk S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                Science 169:56-59(1970).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) me
-!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                  Kohler H., Shimizu A., Paul C., Putnam P.W.; "Macroglobulin structure: variable sequence of light and heavy chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                      Framework-1.
Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.5%; Score 450; DB 1; Length 108; 71.4%; Pred. No. 3.3e-37; Live 19; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-3.
Framework-4.
                                                                                                                                                                                                                                                                                                                                                                                                                  23 Framework-1.
34 Complementarity-determining-
49 Framework-2.
56 Complementarity-determining-
88 Framework-3.
97 Complementarity-determining-
107 Framework-4.
88 By similarity.
88 By similarity.
88 By similarity.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                             SMART; SM00406; TGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 AA
                                                                                                                                                                                                           GO; GO:000576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006952; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
MEDLINE=70201507; PubMed=5447531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    llarity 71.4%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
                                                                                                                                                                         PIR; A01872; K1HUOU.
HSSP; P01607; 1BWW.
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Homo sapiens (Human)
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SEQUENCE
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    SO THE FETT 
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Maddan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., 'Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIOMTOSPSSLSASVGDTVTITCRASQDI----SNYLAWFQQKPGKAPKSLIYGASSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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Biophys. Struct. Mech. 1:139-146(1975).
-!- MISCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain REI.
-! Fegion of the kappa chain REI.
-! MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-! MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocumwager F., oceagemann W., Sonramm H.J.;
"The structure determination of the variable portion of the Bence-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=72189444; PubMed=5028201;
Schischl H., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclona:
immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
Schwager P., Steigemann W., Schramm H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.8%; Score 446; DB 2; Length 23 78.1%; Pred. No. 2e-36; ive 8; Mismatches 13; Indels
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB-Skeletal Muscle;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005332; AAH05332.1;
HSSP; P01834; IHRZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hypothetical protein.
SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
Pfam; PF07654; C1-8et; I.
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                                                                                                                                                              cDNA sequences."
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les 89, Conservative
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P01594;
                                                                                                                                                              and mouse
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2; DWnlee F.E., O'Connor T.P., Benson M.D.; Polymorphism in a kappa I primary (AL) amyloid protein (BAN)."; Mol. Immunol. 23:73-78(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PDB; 1JV5; X-ray; A=1-107.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005953; P:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PR00047; ig; 1.
PROSTTE; PS50835; IG_LIKE; 1.
PROSTTE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th 74.7%; Score 445; DB 1; Length 108; Similarity 79.5%; Pred. No. 1e-36; B9; Conservative 5; Mismatches 14; Indels
                                                                                                                                     Framework-1.
Complementarity-determining-1.
Framework-2.
                                                                                                                                                                         Complementarity-determining-2.
                                                                                                                                                                                                Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11939 MW; E8011187EE6F6FB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-2004 (Rel. 44, Last annotation update)
1G kappa chain V-I region BAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AA
                                                                                                                                                                                                                           By similarity.
                                                                                                                                                                                       Framework-3.
                                                                                                                                                                                                               Framework-4.
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                                                                                                                           Immunoglobulin V region.
DOMAIN 1 23
                                                                                                                                       (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 1
108 1
108 AA;
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Matches 89; Conserv
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                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KV1V HUMAN
P04430;
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Search completed: June 3, 2005, 09:16:13
Job time : 33.7497 secs
                                                                                                                                                                   KV1M HUMAN
P01605;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQLIQSPSSLSASVGDRVTITCRASQSV----YNYVAWFQQKPGKAPKSLIYDASTLQS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and normal
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.4%; Score 443.5; DB 2; Length 107; 79.5%; Pred. No. 1.5e-36; ative 8; Mismatches 10; Indels 5;
                                                                                                                                           Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. Amyloid; Direct protein sequencing; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.7%; Score 445; DB 1; Length 108; 79.5%; Pred. No. 1e-36; Live 8; Mismatches 11; Indels
                                                                                                                                                                                                                                                     Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                  Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                          Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              11840 MW; CD3FD944FE96FD37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035033; AAD56269.1; -.
HSSP; P01607; 1BWW.
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                                                                                                                                                                                                                                                                                                                                                                                    By similarity
                                                                                                                                                                                                                                                                                                                        Framework-3.
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               HSSP; P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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InterPro; IPR001596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIOMIQSPSSLSVSVGDRVTITCQASQNV----NAYLNWYQQKPGLAPKLLIYGASTREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQOSHEDPYTFGQGTKVEIKR 112
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                       GVPSRFSGSGSGTDFTLTISGLQAEDFATYYCQQSY-SALTFGPGTKVDIRR 107
61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Framework-1.
Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 443; DB 1; Length 108;
Pred. No. 1.6e-36;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 Framework-1.
34 Complementarity-determining-
49 Framework-2.
56 Complementarity-determining-
88 Framework-3.
97 Complementarity-determining-
107 Framework-4.
88 By similarity.
108
11834 MW; 739993A95431434A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct protein sequencing; Immunoglobulin V region.

1 23 Framework-1.

DOMAIN 24 34 Complementarity-determ:
                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
18 kappa chain V-I region Lay.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, PO1607, IBWW.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003537; F:antigen binding; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=77038198; PubMed=824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1. __
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity 78.6%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Capra J.D., Klapper D.G.;
                                                                                                                                      STANDARD;
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57
89
98
108
108
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

June Run on:

3, 2005, 08:29:47; Search time 37.3502 Seconds (without alignments) 1180.467 Million cell updates/sec

US-10-791-619-8 596 1 DIQLTQSPSSLSASVGDRVT.....SHEDPYTFGQGTKVEIKRTV 114 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

A_Geneseq_16Dec04:* 1: qeneseqp1980s:* geneseqp1980s:*

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:*geneseqp20000s:* geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Description	Aab76942 Variable	Adn07029 Anti-IgE	_	Aaw95669 Mus muscu	Aab47087 Anti-IgE	Aab76949 Full leng	Aab76951 Full leng	Aab76953 Variable	Aab76958 Variable	Adn07045 Anti-IgE	Adn07036 Anti-IgE	•	Adn07040 Anti-IgE	Aaw95653 Mus muscu	Aaw95660 Mus muscu	Aaw95662 Mus muscu	_	Aab07472 Amino aci	Aab74211 E27 anti-	Abu62797 E27 anti-	_	Adf29038 Anti-IgE	Aaw95668 Mus muscu	Aaw95667 Mus muscu	Aab76957 SFv fragm
ΙD	AAB76942	1 ADNO7029	: AAW95664	: AAW95669	AAB47087	AAB76949	AAB76951	AAB76953	AAB76958	3 ADN07045	3 ADN07036	1 ADN07038	3 ADN07040	: AAW95653	: AAW95660	: AAW95662	: AAY50030	AAB07472	AAB74211	. ABU62797	, ADF69597	, ADF29038	: AAW95668	: AAW95667	AAB76957
Length DB	114 4	114 8	218 2	218 2	218 4	218 4	218 4	218 4	218 4	218 8	218 8	218 8	218 8	114 2	218 2	218 2	218 2	218 3	218 4	218 6	218 7	218 7	248 2	248 2	248 4
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	7.66	7.66	7.66	7.66	99.7	99.7	99.7	7.66	99.7	98.5	98.5	98.5
Score	296	296	296	296	296	296	296	296	296	596	296	296	296	594	594	594	594	594	594	594	594	594	587	587	587
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Aab76956 SFV fragm Adn07044 Anti-IgE Adn07043 Variable Adn07030 Anti-IgE Adn07066 F(ab)-Bha Aaw55655 Mus muscu Aaw5655 Mus muscu Aaw5655 Mus muscu Aaw5658 Mus muscu Aaw5658 Mus muscu Aaw95609 Musriable Adn07031 Anti-IgE Aaw95609 Anti-IgE Adn07034 Anti-IgE Adq90719 Anti-IgE Adq90719 Anti-IgE Adq90719 Anti-IgE Adq90719 Anti-IgE Adq90719 Anti-IgE Adq90719 Anti-IgE Adq90719 Anti-IgE Adq90719 Anti-IgE Adq90719 Anti-IgE	_
AAB76956 ADN07044 AADN07044 AAN07043 AAN07030 AAN05655 AAW95655 AAW95658 AAW95658 AAW95658 AAW956719 AAW950719 AAW950719 AAR33312 AAR33312	ADN07027
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5847 5847 5870 5770 5770 5770 5770 5770 5770 577	556
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	45

ALIGNMENTS

AAB76942 standard; protein; 114 AA. RESULT 1 **AAB**76942

AAB76942;

(first entry) 17-APR-2001

Variable light chain sequence of e26 and e27 SEQ ID 8.

Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.

Synthetic.

US6172213-B1.

09-JAN-2001.

98US-00109207. 30-JUN-1998; 97US-0051554P. 02-JUL-1997;

(GETH) GENENTECH INC.

Lowe J; Jardien PM, Lowman HB, Presta LG,

WPI; 2001-122353/13.

New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity maturation with phage display.

Disclosure; Fig 2; 87pp; English.

This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgE antibody activity. The antibody has improved action due to a process comprising, a) identifying aspartyl residues prone to isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic; ophthalmological; dermatological and antiniflammatory activity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned

anaphylactic hypersensitivity and asthma, allergic rhinitis and

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               diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76936-AAB76900 represent fragments of anti-1gs antibodies of the invention. Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-1gs antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition of an improved anti-1gE antibody or 1gE binding fragment, useful for treating 1gE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
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                                                                                                                                                                                                                1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                      1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
acids may also be used as affinity purification agents and in
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                           61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                              GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder; therapy; attopic allergy; anaphylactic hypersensitivity; asthma; allergic rhintis; conjunctivitis; eczema; urticaria; food allergy; variable light chain domain; VL.
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-IgE antibody e26 and e27 variable light chain domain (VL).
                                                                                                                                                    Query Match 100.0%; Score 596; DB 4; Length 114; Best Local Similarity 100.0%; Pred. No. 1.2e-35; Matches 114; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 8; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jardien PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     ADN07029 standard; protein; 114 AA.
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/label= CDR-L2
93..100
/label= CDR-L3
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/label= CDR-L1
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-326922/30.
                                                                                                                        Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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                                                                                                                                                                                                                                                                                                                                                     RESULT 2
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The invention relates to therapeutic compositions comprising anti-IgB antibody or IgB blinding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgB-mediated disorders. The disorders include atopic allergy associated with

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                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of the variable light Fab fragment of e26 and e27. It was used as part of a method to improve the affinity of anti-1gE antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgE mediated production of histamine in a mammal. They can be used for treating a disorder mediated by IgE such as hypersensitivity, atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable light Fab fragment, antibody; anti-IgE, reduction; prevention; bistamine; production; hypersensistivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria; IgE.
                                                                                                                                                                                                       1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                        DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                      Gaps
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                                                                                                                                                                                                                                          61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                            61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQOSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus anti-1gE e26 & e27 variable light chain Fab fragment
                conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-1gE antibody variable light chain domain (VL)
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                                                                                                Length 114;
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                                                                                                  100.0%; Score 596; DB 8;
100.0%; Pred. No. 1.2e-35;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 99-100; 129pp; English.
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                                                                                                                                                                                                                                                                                                                                                             AAW95664 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US013410
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                               Query Match
Best Local Similarity 100.
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-106057/09.
                                                                  Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  )2-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9901556-A2
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(first entry)

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Light chain; heavy chain; anti-IgE antibody; E26; transfection; green fluorescent protein; GFP; promoter; expression.
                                                                                       Anti-IgE antibody, E26, light chain.
           AAB47087 standard; protein; 218 AA
                                                                                                                                                                                                                                        11-JUL-2000; 2000WO-US018841.
                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                            WO200104306-A1
                                                                                                                                                                                                                                                               12-JUL-1999;
                                                                                                                                                           musculus
                                                      11-SEP-2003
08-MAY-2001
                                                                                                                                                                                                                  18-JAN-2001.
                                  AAB47087;
                                                                                                                                                                     Chimeric.
                                                                                                                                                Ношо
                                                                                                                                                            Mus
                        Improving affinity of polypeptides, particularly anti-IgE antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of the variable light chain F(ab)'2 fragment of e26 and e27. It was used as part of a method to improve the affinity of anti-
IgB antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgB mediated production of histamine in a mammal. They can be used for treating a disorder mediated by IgB such as hypersensitivity, atogic allergy, asthma, allergic thinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and
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Variable light chain; IgE; antibody; anti-IgE; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria; F(ab)'2 fragment.
                                                                                                                                                                                           Mus musculus anti-IgE e26 & e27 variable light chain F(ab)'2fragment.
                                                       GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV
                                                                                                                                                                                                                                                                                                                                                                                                               Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 104; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Jardieu PM,
                                                                                                                        AAW95669 standard; protein; 218 AA
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                                                                                                                                                                    08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-106057/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                           30-JUN-1998;
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                                                                                                                                                                                                                                                                                                WO9901556-A2
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                                                                                                                                                                                                                                                                                                                                                                                                             Lowman HB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis
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99US-0143360P.

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The sequences given in AAB47087-88 represent the light and heavy chains of the anti-1gE antibody, E26. These sequences were expressed by the construct of the invention, which comprises an amplifiable selectable gene, a green fluorescent protein gene (GFP), and a selected sequence encoding a desired product, which is operably linked to either the amplifiable selectable gene or to the GFP gene, and to a promoter. Constructs such as this, are useful for producing a desired product by introduction into a suitable eukaryotic cell, culturing the resultant eukaryotic cell under conditions so as to express the desired product, and recovering the desired product from the culture medium. The constructs are efficient for identifying and selecting for stable constructs are efficient for identifying and selecting for stable suitable for earlier and faster screening of transfected cells. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                     Novel polynucleotide construct for screening and obtaining cells expressing high levels of desired protein, comprises amplifiable selectable gene, fluorescent protein gene and sequence encoding desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
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Meng YG;
   Krummen LA,
                                                                                                                                                                                                                                                                                       Disclosure; Fig 13A; 75pp; English.
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Matches 114; Conservative
Crowley CW,
                                                               WPI; 2001-138352/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 218 AA;
Chisholm V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                 product.
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ID AAB7
XX
AC AAB7
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1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES 1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES

100.0%; Score 596; DB 2; Length 218; 100.0%; Pred. No. 2.1e-35; ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 114; Conservative

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GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDFYTFGGGTKVEIKRTV 114

RESULT

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Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.
                                                                                                                                                                                                                                    New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity
                           Full length light chain sequence of e26 SEQ ID 15.
                                                                                                                                                                                                 Jardieu PM,
                                                                                                                                                                                                                                                                                    Claim 2; Fig 12; 87pp; English.
                                                                                                                                                                                                                                                                   maturation with phage display
                                                                                                                                           98US-00109207.
        (first entry)
                                                                                                                                                                                                  Lowman HB, Presta LG,
                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                    WPI; 2001-122353/13.
                                                                                                     US6172213-B1
                                                                                                                                          30-JUN-1998;
                                                                                                                        09-JAN-2001
                                                                                   Synthetic
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This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgB antibody activity. The antibody has improved action due to a process comprising, a) identifying separtyl residues prone to isomerisation in unimproved anti-IgB (immunoglobulin B) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiathmatic; antiallergic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgB-mediated disorders couch as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in specific cell, tissues or serum. Amino acid sequences AABNF036.

AABNF606 represent fragments of anti-IgB antibodies of the invention. Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-IgE antibodies

Sequence 218 AA;

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                                                                                                         1 DIQLIQSPSSLSASVGDRVTITCRASKPVDGEGDSYLAWYQQKPGKAPKLLIYAASYLES
                                                                                   1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                             Gaps
                                                                                                                                                                     61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                          GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQCTKVEIKRTV 114
                                             ö
100.0%; Score 596; DB 4; Length 218; 100.0%; Pred. No. 2.1e-35; ive 0; Mismatches 0; Indels (
                     Best Local Similarity 100. Matches 114; Conservative
    Query Match
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AAB76951 standard; protein; 218 AA 17-APR-2001 (first entry) AAB76951; RESULT 7 AAB76951 UXXXE/

Variable light chain Fab fragment of e26 and e27 SEQ ID 19.

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improved anti-IgE antibody activity. The antibody has improved action due to a process comprising, a) identifying asparryl residues prone to show a process comprising, a) identifying asparryl residues prone to substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic; ophthalmological, dermatological and antiinflammatory activity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic are useful for treating IgE-mediated disorders food allergies. The muteant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antigen of interest an specific cell, tissues or serum. Amino acid sequences AAB76936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-IgB antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a nucleotide sequence encoding an antibody with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                     Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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                 Full length light chain sequence of e27 SEQ ID 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 596; DB 4;
100.0%; Pred. No. 2.1e-35;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Fig 12; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  maturation with phage display
                                                                                                                                                                                                                                                98US-00109207
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                                                                                                                                                                                                                                                                                                                                                                 Presta LG,
                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 218 AA;
                                                                                                                                                                                                                                                30-JUN-1998;
                                                                                                                                                                                                                                                                                     02-JUL-1997;
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                                                                                                                                Synthetic.
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Matches
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Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig B; immunoglobulin B; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.
                                                           98US-00109207.
                                                                     97US-0051554P.
                                                                                           Presta LG,
                                                                                (GETH ) GENENTECH INC
                                                                                                      WPI; 2001-122353/13.
                                     US6172213-B1
                                                          30-JUN-1998;
                                               09-JAN-2001
                                                                                          Lowman HB,
                           Synthetic
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New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity maturation with phage display

Lowe

Jardieu PM,

Claim 1; Fig 13; 87pp; English

This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgE antibody activity. The antibody has improved action due to a process comprising a) identifying asparty1 residues prone to isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic, ophthalmological, dermacological and antiinflammatory activity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, unticaria and food allergies. The mutant antibodies produced by the above mentioned nucleic assays for detecting the expression of an antigen of interest in anticity assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76936-AAB76960 represent fragments of anti-IgE antibodies of the invention. Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-IgE antibodies

Sequence 218 AA;

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                                                                                                                   1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                              1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                        Gaps
                                                                                                                                                           GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                             GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
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100.0%; Score 596; DB 4; Length 218; 100.0%; Pred. No. 2.1e-35;
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                                    0; Mismatches
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                    Best Local Sim
Matches 114;
  Query Match
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AAB76958 standard; protein; 218 17-APR-2001 (first entry) AAB76958; RESULT 9 AAB76958 **EXEXEXEX**

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Variable light chain F(ab)'2 fragment of e26 and e27 SEQ ID 24.

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Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
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improved anti-19E antibody activity. The antibody has improved action due to a process comprising, a) identifying aspartyl residues prone to isomerisation in unimproved anti-19E (immunoglobulin E) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic; ophthalmological, dermatological and antiinflammatory activity. The antibodies are useful for treating 19E-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in apportic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76916-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asmid used in
AAF69271 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a nucleotide sequence encoding an antibody with
                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of anti-IgE antibodies of the invention.
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antiinflammatory, Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide sequence AAF69253 represents an expression plasmid the course of the invention, and oligonucleotides AAF69254 - AAF69 used in the generation of affinity improved anti-1gE antibodies
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                                                                                                                                                                                                                                                                                                             Lowe
                                                                                                                                                                                                                                                                                                           Jardien PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 15; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      maturation with phage display
                                                                                                                                                                                     98US-00109207.
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                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
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                                                                                                                                                                                   10-JUN-1998;
                                                                                                                                                                                                                            02-JUL-1997;
                                                                                                      JS6172213-B1
                                                                                                                                             19-JAN-2001.
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Anti-IgE antibody e26 and e27 variable light (VL) F(ab)' 2 fragment Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder; therapy; atopic allergy; anaphylactic hypersensitivity; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy; Z ADN07045 standard; protein; 218 (first entry) 01-JUL-2004 ADN0704 **EXXXXXXXXXXX**

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New composition of an improved anti-IgE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
                                                                                                                                                     New composition of an improved anti-IgE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
                                                                                                                                                                                                                                                                The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable light chain (VL).
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                                                                               Lowe
                                                                                                                                                                                                                                Claim 1; SEQ ID NO 15; 89pp; English.
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                                                                             Jardien PM,
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98US-00109207
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                                                                           Presta LG,
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                                       (GETH ) GENENTECH INC
                                                                                                                 WPI; 2004-326922/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 218 AA;
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 30-JUN-1998;
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30-JUN-1998;
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                                                                             Lowman HB,
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                                                                                                                                                                                                                                                                                                                                                                  New composition of an improved anti-1gE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticar and food allergies. The present sequence is an anti-IgE antibody variable light chân (VL) F(ab)' 2
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                                                                                                                                                                                                                                                                                          Lowe J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; SEQ ID NO 24; 89pp; English.
                                                                                                                                                                                                                                                                                          Jardien PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADN07036 standard; protein; 218 AA
                                                                                                                                                     17-NOV-2000; 2000US-00716028.
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variable light chain; VL
                                                                                                                                                                                                                                                                                          Presta LG,
                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                     Unidentified
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RESULT 11 ADN07036

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Gaps

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Mismatches

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114; Conservative

Similarity

Length 218;

Score 596; DB 8; Pred. No. 2.1e-35;

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61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114

(first entry)

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Variable light chain, IgB; antibody; anti-IgB; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
                                                                                                                                                                                                                                            Mus musculus anti-IgE e26 & e27 variable light chain.
                                                                                                                                                                          AAW95653 standard; protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
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                     The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allersy associated with amaphylactic hyporsensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable light chain (VL).
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                                                                                                                                                                                                                                                                                                                                                                                                        Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder; therapy; atopic allergy; anaphylactic hypersensitivity; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
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                                                                                                                                                                                                                                                                                                                                                                                     Anti-IgE antibody e26 and e27 variable light (VL) Fab fragment.
                                                                                                                                       Length 218;
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                                                                                                                                      100.0%; Score 596; DB 8;
100.0%; Pred. No. 2.1e-35;
tive 0; Mismatches 0;
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SEQ ID NO 17; 89pp; English.
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                                                                                                                                                  Similarity
                                                                                                                Sequence 218 AA;
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97US-00887352

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                                                                                                                                                                                                                                                                                                                                              The sequence is that of the variable light chain of e26 and e27. It was used as part of a method to improve the affinity of anti-IgB antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgB mediated production of histamine in a mammal. They can be used for treating a disorder mediated by IgB such as hypersensitivity, excipt allergy, asthma, allergic thinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and diagnosis
                                                                                                                         Improving affinity of polypeptides, particularly anti-IgB antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQLIQSPSSLSASVGDRVTITCRASKPVDGEGDSYMNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.7%; Score 594; DB 2;
99.1%; Pred. No. 1.6e-35;
ive 1; Mismatches 0;
   Lowe J;
                                                                                                                                                                                                                                                                                               Disclosure; Page 89; 129pp; English.
Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 113; Conservative
Lowman HB, Presta LG,
                                                            WPI; 1999-106057/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable light chain (VL) Pab fragment.

Sequence 218 AA;

Claim 7; SEQ ID NO 19; 89pp; English.

RESULT 15

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The sequence is that of the full length light chain of e26. It was used as part of a method to improve the affinity of anti-IgE antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgE mediated production of histamine in a mammal. They can be used for treating a disorder mediated by IgE such as hypersensitivity, actor, asthma, allergic thinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Improving affinity of polypeptides, particularly anti-IgE antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                          Light chain; IgB; antibody; anti-IgB; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
                                                                                                               Mus musculus anti-IgE e26 full length light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                              Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 94-95; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Jardieu PM,
               AAW95660 standard; protein; 218 AA
                                                                                                                                                                                                                                                                                                                               98WO-US013410.
                                                                                                                                                                                                                                                                                                                                                              97US-00887352.
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-106057/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 218 AA;
                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                               WO9901556-A2
                                                                                                                                                                                                                                                                                                                             30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                              02-JUL-1997;
                                                                                 08-JUN-1999
                                                                                                                                                                                                                                                                                             14-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            Lowman HB,
                                                 AAW95660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             target.
AAW95660
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Query Match 99.7%; Score 594; DB 2; Length 218; Best Local Similarity 99.1%; Pred. No. 2.9e-35; Matches 113; Conservative 1; Mismatches 0; Indels 0; Gaps

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8 8 8

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Search completed: June 3, 2005, 09:09:07 Job time: 38.3502 secs

	Ltd.
5.1.6	Compugen
version	- 2005
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

June Run on:

3, 2005, 08:53:28 ; Search time 7.09576 Seconds (without alignments) 1545.812 Million cell updates/sec

US-10-791-619-11

score: Title: Perfect :

623 1 EVQLVESGGGLVQPGGSLRL.....YCARGSHYFGHWHFAVWGQG 114 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:* Database

pir1:* pir2:* 3: pir3:* 4: pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	***************************************			heavy chain	heavy	heavy		cha		heavy chain V		heavy chain V	heavy chain -	heavy chain -	Ig heavy chain V r	heavy		heavy	heavy chain -	heavy	heavy chain V	Ig heavy chain V r		heavy chain V		heavy chain pr		heavy chain V	heavy cha	heavy chain -
SUMMAKIES	E		S31588	S70442	S31114	S31666	S31113	137780	E36005	S48797	S31669	830531	836259	S31107	S31117	S19666	G36005	S31598	831686	S38489	S31701	S26794	S20782	ന	S31587	S31108	S05271	D36005	a	831603	ς.
	EC	1	7	~	C3	7	~	N	N	~	~	N	~	~	~	0	N	~	N	N	~	7	~	N	~	7	~	~	0	~	7
	Length		140	140	123	138	121	147	122	128	141	125	117	119	122	121	121	135	140	127	137	123	124	114	136	119	160	119	143	132	116
	Query Match		-	67.2	-	8.99	66.3	66.1	65.7	65.7	65.7	65.5	65.3	65.3	64.9	64.8	4	4	64.8	64.7	64.4	4	Z.	64.1	4		4	63.9	63.9	<u>.</u>	63.6
	Score		419	418.5	418	416	413	411.5	409.5	409.5	409.5	408	407	407	404.5	404	404	404	404	403	401.5	401	400.5	399.5	99	399	399	398	398	'n	396.5
	Result No.		н	Ŋ	٣	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig heavy chain V-I	ig heavy chain V r	Ig variable region	Ig heavy chain - h	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain - h	Ig heavy chain V r	Ig heavy chain V r	anti-tetanus toxin	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V-I	Ig heavy chain V r	. Ig heavy chain V r
M.	-1		9	8	4	2	Ę.	6	0	60	2	6	∑:	0	9
M3HUE	83160	137781	83111	S4879	83167	C36005	15567	831699	846390	PC2398	F36005	831679	M3HUA	S26790	S78486
1 M3HUE				2 S4879						2 PC239			_	٠.	2 S7848
120 1 M3HUE	~	~	7	7	0	7	7	~	N	N	~	7	-	N	7
н с	130 2	139 2	118 2	120 2	139 2	119 2	121 2	134 2	114 2	122 2	119 2	134 2	122 1	128 2	117 2
120 1	63.6 130 2	63.6 139 2	63.5 118 2	120 2	63.5 139 2	63.4 119 2	121 2	63.4 134 2	114 2	122 2	119 2	63.2 134 2	122 1	63.2 128 2	117 2

ALIGNMENTS

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Using heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the fargeternce number: S31588
A;Reference number: S31588
A;Reference preliminary
A;Residues: 1-140 <CUI>A;Gross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 EVQLLESGGGGLVQPGGSLRLSCAASGFTFSS-YAMSWVRQAPGKGLEWVSA1SGSGGSTY
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Best Local S:
Matches 82
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RESULT 2 S70442

Ig heavy chain precursor V region (mu) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Uul-1998 #sequence_revision 24-Uul-1998 #text_change 09-Uul-2004
C;Accesianier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
A;Title: IgM kapps/lambda EBV human B cell clone: an early step of differentiation of fet A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Reference number: occompared with conceptual translation

A;Molecule type: mRNA A;Residues: 1-140 <CUI> A;Cross-references: UNIPROT:Q8WUKI C;Superfamily: immunoglobulin V region; immunoglobulin homology F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 418.5; DB 2; Length 140; Best Local Similarity, 72.2%; Pred. No. 2.7e-30;

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C; Accession: S31113

R; Raaphoret, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Bur. J. Immunol. 22, 247-251, 1992

Bur. J. Immunol. 22, 247-251, 1992

A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme A; Reference number: S31104; MUID: 92111633; PMID: 1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: 137780; S25474
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; MUID:94119917; PMID:8290556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X62962
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSS-YAMSWVRQAPGKGLEWVSAISGSGGSTY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVOLVESGGGLVQPGGSLRLSCAASGFTFSS-YMMSWVRQAPGKGLEWVANIKQDGSEKY 72
                                                                                                                                                                                                                                                                                                                                                                             A, Accession: S11113
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK- 59
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: E36005
                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYS-GETK
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  79 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAR--TGYWYFDLWGRG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579 C;Superfamily: immunoglobulin V region; immunoglobulin homology <I,MM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig variable region (VDJ) (clone T20-11) - human (fragment)
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 66.3%; Score 413; DB 2; Local Similarity 70.4%; Pred. No. 7.2e-30; les 81; Conservative 13; Mismatches 19
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A, Residues: 1-147 < RES>
                                                                                                                                              Ig heavy chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: S31114
Stanborset, F. M., Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S31666
K:Cuisinier, A.W.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991 C;Superfamily: immunoglobilin V region; immunoglobilin homology C;Keywords: heterotetramer; immunoglobilin P;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S31114
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Species: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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Ig heavy chain V region - human (fragment)
IS heavy elone sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHY--FGHWHFAVWGQG 114
                                                                                            20 QVQLVESGGGGVVQPGGSLRLSCAASGFTF-SNYGMFHWVRQAPGKGLEWVAFIRYDGSNKY
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                                                           EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK-
     3; Gaps
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                                                                                                                                                                                                       YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
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  20; Indels
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  9; Mismatches
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  Conservative
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Best Local Similarity
Matches 84; Conserv
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A;Residues: 1-138 <CUI>
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S31669
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the RMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the & A;Reference number: S31585
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C;Accession: S36259
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 7152-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 EVQLVESGGGLVKPGGSLRLSCAASGFTFSS-YSMNWVRQAPGKGLEWVSSISSSSYIY 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S30531
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Accession: S30531
A;Accession: S30531
A;Status: preliminary
A;Molecule type: mRNAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGH-WHFAVWGQG 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.7%; Score 409.5; DB 2; Length 141; llarity 70.7%; Pred. No. 1.7e-29; Conservative 12; Mismatches 19; Indels 3;
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A,Ross-references: UNIPROT:Q9UL91; EMBL:218317
A,Cross-references: UNIPROT:Q9UL91; EMBL:218317
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
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69.2%; Pred. No. 2.18-29;
iive 11; Mismatches 18; Indels
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A,Molecule type: mRNA
A,Residues: 1-141 <CUI>
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82;
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Best Local S:
Matches 82
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R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Fitle: enumber: A36005; MUID:90349571; PMID:2117273
A;Accession: B36005
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R;Tomlinson, 1.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Moll Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
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C;Species: Homo sapiens (man)
C;Dacession: 348797; $256893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the RML Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: $48797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.7%; Score 409.5; DB 2; Length 122; 70.1%; Pred. No. 1.5e-29;
                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                       A; Cross-references: GB: M34030
                                                                                                                                           A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-122 <SCH>
                                                                                                                                                                                                                                                                                A;Gene: GDB:IGH@; IGHDY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-128 < MAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-98 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 QG 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S26893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82;
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Best Local S
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59

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Length 122;

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C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accespino: S19666
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Tille: By-passing immunization. Human antibodies from V-gene libraries displayed on ph: A;Reference number: S19663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene s
A;Reference number: A36005; MUID:90349571; PMID:2117273
                                                                                                                                                                        1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK- 59
                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Spate: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVOLVESGGGLVOPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDFFAPPNWSHFDYWGGG 115
                                                                                                                                                                                                                                                                                            60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHW-HFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.8%; Score 404; DB 2; Length 121; Best Local Similarity 68.7%; Pred. No. 4.6e-29; Matches 79; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroteramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                 22; Indels
                                                DB 2;
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                                                   Score 404.5; DB 2
Pred. No. 4.1e-29;
                                                                                                              9; Mismatches
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region (VH3DJH4) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (M74) - human
                                                       ch 64.9%;
1 Similarity 70.7%;
82; Conservative
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                                                       Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-121 < MAR>
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A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
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S19666
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C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S31107
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31107
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-119 <RAA>
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A;Cross-references: EMBL:X62967
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Stywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Cross-references: EMBL:X62955
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFG----HWHFAVWGQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCAR--GSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK-
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                                                                                                              A, Cross-references: EMBL:Z18850; NID:g33123; PIDN:CAA79302.1; PID:g939902 C.Superfamally: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:15-98/Domain: immunoglobulin homology <NM>
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                                                                                                                                                                                                                                                                                                                       21; Indels
                     A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA
A;Residues: 1-117 <GRI>
                                                                                                                                                                                                                                                             Query Match 65.3%; Score 407; DB 2; Best Local Similarity 68.6%; Pred. No. 2.4e-29; Matches 81; Conservative 10; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 65.3%; Score 407; DB 2;
1 Similarity 70.9%; Pred. No. 2.4e-29;
83; Conservative 12; Mismatches 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 83; Conserv
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A; Accession: S36259
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Search completed: June 3, 2005, 09:17:50 Job time: 7.09576 secs g

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June Run on:

3, 2005, 08:31:37 ; Search time 32.7497 Seconds (without alignments) 1782.523 Million cell updates/sec

Title: Perfect score:

US-10-791-619-11 623 1 EVQLVESGGGLVQPGGSLRL......XCARGSHYFGHWHFAVWGQG 114 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

1612378

1612378 seqs, 512079187 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* ٠. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	nescribiton	Q6pja4	. Q9u190	Q6in78	Q6pi81	Q9u172	P01766	Q8wuk1	Q65zc9	Q6n089	P01768	Q9u191	Q6mzv7	Q6gmy2	6qq960	Q6mzg6	Q9u193	Q9u171	Oemzne	P01793	P19181	Q8wu38	Q9y509	P01764	Q6gmx2	Q96k68	Q9hcc1	Q8nc16	P01767	P01791	Q8n5k4	07770
	TT	Q6PJA4	Q9UL90	Q61N78	Q6P181	Q9UL72	HV3E HUMAN	Q8WUK1	0652C9	06N089	HV3G HUMAN	Q9UL <u>9</u> 1	Q6MZV7	Q6GMY2	Q96BB9	06MZQ6	Q9UL93	Q9UL71	O6MZU6	HV24 MOUSE	HV05 CARAU	Q8WU38	Q9Y509	HV3C HUMAN	Q6GMX2	Q96K68	Q9HCC1	QBNCL6	HV3F HUMAN	HV22_MOUSE	Q8N5K4	TARREST TOTAL
g	9 :	7	7	N	7	7	-	7	7	7	ч	N	~	7	7	~	N	0	0	ч	7	N	7	7	7	7	7	7	П	٦	0	-
1	match bength	470	113	466	478	118	120	613	240	472	122	118	473	909	597	475	116	121	464	123	116	573	147	117	493	494	112	493	115	123	499	0
Query	Maccin	66.3	65.5	64.0	63.9	63.8	63.6	63.3	63.2	63.2	63.2	63.0	62.8	62.8	62.8	62.5	62.4	62.4	62.4	61.8	61.7	61.6	61.4	61.3	61.2	61.1	9.09	60.5	0.09	0.09	0.09	2
	acore	413	408	399	398	397.5	396	394.5	394	394	393.5	392.5	391.5	391.5	391	389.5	389	389	389	385	384.5	383.5	382.5	382	381	380.5	377.5	377	374	374	374	27.0
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Q80ZI7 HV3J HUMAN	HV20_MOUSE Q6MZV6	Q6ZVX0 Q7Z5W1	HV3B_HUMAN	HV21 MOUSE	Q99KA4	HV18 MOUSE	HV23 MOUSE	HV19 MOUSE	HV46 MOUSE	HV30_MOUSE
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487	122 479	487	114	122	487	123	123	123	137	113
59.6	59.3 59.1	59.1 58.9	58.8	58.8	58.8	58.6	58.6	58.4	58.4	58.3
371 370	369.5 368.5	368.5 367	366.5	366.5	366.5	365	365	364	364	363
332	6. 6. 4. 7.	36 37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
X Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
XA Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
XA Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.E., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
Detchenco, L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,
XA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
XA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rouffard G.G.,
A Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
XA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
XA Gones S.J., Marra M.A.;
XI "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                               Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Primary B-Cells;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO18747; AAH18747.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                        470 AA.
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InterPro; IPR003599; IG.
InterPro; IPR00310; IG_1ike.
InterPro; IPR003597; IG_2.
InterPro; IPR003596; IG_0.
InterPro; IPR003596; IG_0.
InterPro; IPR004596; IG_0.
InterPro; IPR00459; IG_0.
InterPro; IPR00459; IG_0.
INTERT; SM00407; IGC1; 3.
SMART; SM00407; IGC1; 3.
INTERT; PS50835; IG_IKE; 4.
PROSITE; PS50835; IG_IKE; 4.
                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.
                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                             Q6PJA4;
                                    Q6PJA4
Q6PJA4
                                                                             DOTAL SERVICE SERVICE
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64.0%;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC072419; AAH72419.1;
HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.33,
Best Local 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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      NCBI_TaxID=9606;
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      SOR REAL PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
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                                                                                                                                                                                                                                                             1 BVQLVESGGGVVQPGGSLRLSCAASGFTFSS-YGMHWVRQAPGKGLEWVAFIRYDGSNKY
                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY
                                                                                                                                                                                                                                                                                                                                                                                    79 YVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWYRDW-FDPWGQG 133
                                                                                                                                                                                                                                                                                                                                                   61 N-PSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCAR-GSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.5%; Score 408; DB 2; Length 113;
Best Local Similarity 70.4%; Pred. No. 8.2e-34;
Matches 81; Conservative 10; Mismatches 14; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK-
                                                                                                                                                              4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                            Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myosin-reactive immunoglobulin heavy chain variable region
                                                                                         cch 66.3%; Score 413; DB 2; Length 47 al Similarity 72.4%; Pred. No. 1.2e-33; B4; Conservative 11; Mismatches 17; Indels
Hypothetical protein.
SEQUENCE 470 AA; 51715 MW; 7B49556AllFD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 AA; 12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clin. Immunol. Immunopathol. 87:184-192 (1998)
                                                                                                                                                       11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROSITE; PS50835; IG LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UL90;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                             Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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Name=IGHG1;
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SEQUENCE
                                                                                            Query Match
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Q9UL90
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20 EVQLVESGGGLIQPGGSLTLSCAASGLTVSSNY-MHWVRQAPGKGLEWVSVLYIGGATYY 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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| InterPro; | IRR0013599; | 19-1ike. |
| InterPro; | IRR0031095; | 19-1ike. |
| InterPro; | IRR0030065; | 19-1ike. |
| InterPro; | IRR004005; | 16-1ike. |
| InterPro; | IRR004005; | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Peripheral Nervous System;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last sequence update)
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k; Pred. No. 3.2e-32;
11; Mismatches 20;
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"Myosin-reactive autoantibodies in rheumatic carditis and normal
         WEDLINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wa X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                         118 118
118 AA; 12872 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
                                                                                                                                                                              Similarity 72.2
83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 80; Conserv
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   HV3E HUMAN
                                                                                                                                         NON_TER
SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                      Query Match
                                                Fetus.";
                                                                                                                                                                                 Local
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      61 N-PSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCAR-----GSHYFGHWHFAV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 YVDSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCAREFESTMTTVNADYY-YFYMDV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YWMSWVRQAPGKGLEWVANIKQDGSEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                      63.9%; Score 398; DB 2; Length 478;
65.3%; Pred. No. 4.2e-32;
.ive 15; Mismatches 16; Indels 12;
MEDLINE=22388257; Pubmed=1247.7932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                             Strausberg R.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC041037; AAH41037.1; -. HSSP; P01861; IADQ.
                                                                                                                                                                                                                                                                                                                          SWART; SM00409; IG; 2.
SWART; SM00407; IGc1; 3.
SWART; SM00407; IGc1; 3.
SWART; SM00406; IGv; 1.
PROSITE; PS0035; IG_MC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;
                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 118 AA
                                                                                                                                                                                                                                                                   InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-set; 3.
                                                                                                                                                                               and mouse cDNA sequences."
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Hes 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                     IISSUE=Primary B-Cells;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 WGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 WGKG 141
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Q9UL72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNY-MNWVRQAPGKGLESV-SVTYSGGSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capra J.D., Hopper J.E.;
"Comparative studies on monotypic IgM lambda and IgG kappa from an "Comparative studies on monotypic IgM lambda acid sequence of the VH region of the IgM paraprotein.";
Immunochemistry 13:925-999(1976).
-!- MISCELLANBOUS: This chain was obtained from IgM isolated from the serum of a patient with malignant lymphoma of the Waldenstrom
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 YADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAPYYCARDR--FGEFLFDYWGQG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=77117674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;
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                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 118;
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                                                                                                                                                                                                                                                                                                                                                      63.8%; Score 397.5; DB 2; Length 72.2%; Pred. No. 1e-32; ive 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02049; MBHUBW.
HSSP; P01783; IIGC.
GO; GO:000576; C:extracellular; NAS.
GO; GO:0005576; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;
                                                                                                                                                                                                                                                                                                    B4D1A5944B2D5CCA CRC64;
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65.0%; Pred. No. 1.5e-32;
iive 12; Mismatches 17;
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AP035042; AAD56278.1; -.
PIR; S21205; S21205.
HSSP; P01783; 11GC.
InterPro; IPR001110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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21-JJJ-1986 (Rel. 01, Last sequence update)
05-JJJ-2004 (Rel. 44, Last annotation update)
Homo sapiens (Human).
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613 AA; 67295 MW; 60C7F5950671E315 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Single-chain Fv (Fragment)
                                                                             80; Conservative
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=scFv;
  SQ SEQUENCE
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Q6N089;
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1D Q6
AC Q6
DT Q5
DT 05
DT 05
DT NA
GN NA
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIJURE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RAIschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Staptecon M., Soares M.B., Bornaldo M.F., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahe J., Helton E., Ketteman M., Madan A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Dones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                 111
                                                                                                                                   60 ADSVKGRFTISRNDSKNTLYLNMNSLRAEDTAVYYCARSPVSLVDGWLYYYYG----SVW 115
                    9
                                          1 EVQLVESGGGLVQPGGSLRLSCAASGFTF-SYYNMWWVRQVTGKGLEWVSAIGTAGDQYY 59
                    EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY
                                                                                               61 NPSVKGRITISRDDSKNIFYLOMNSLRAEDTAVYYCARGS------HYFGHWHFAVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-Primary B-Cells,
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                613 AA.
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Pfam; PF07654; Cl-set; 4.
SMART; SMO0406; IQ., 1.
PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                PRT;
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PIR; G36005; G36005
PIR; PH1643; PH1642.
PIR; PH1643; PH1645.
PIR; PH1645; PH1646.
PIR; PH10908; PL0098
PIR; PL0120; PL0120
PIR; S31116; S31116
PIR; S311116; S31119
PIR; S311116; S31119
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S31119.
S70442.
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                                                                                                                                                                          112 GQG 114
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60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWH-----FAVWGQG 114
                                                                                                                                                                                                                                                                                                         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSS-YGMHWVRQAPGKGLEWVAVISYDGSNKY 78
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                                                                                                                                  Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                            13;
            Length 613;
                                                                                                                     17; Indels
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686F15220.
Name=DKFZp686F15220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
      DB 2;
Score 394.5; DB 2
Pred. No. 1.3e-31;
                                                                                                                     10; Mismatches
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      63.3%;
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122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.";
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NON TER
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                                                                                                                                                                                                                                                                                                                           Q9UL91
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Q6MZV7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKY-SGETK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCAR--GSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                             The German Human cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Fabo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640627; CAE45781.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lehman D.W., Putnam F.W.,
"Amino acid sequence of the variable region of a human mu chain:
location of a possible JH segment.".
Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
-!- MISCELLANBOUS: This mu chain was isolated from the plasma of
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.2%; Score 394; DB 2; Length 472; Best Local Similarity 66.7%; Pred. No. 1.1e-31; Matches 78; Conservative 14; Mismatches 21; Indels
                                                                                                                                          HSSP, PO1861, TAGAS, TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrrolidone carboxylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patient with macroglobulinemia.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02051; M3HUAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, PO1772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=81013859; PubMed=6774332;
                                       ISSUE=Human rectum tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
                     SEQUENCE FROM N.A.
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P01768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGET-K 59
                                                                                                                                                  1 QVELVESGGGVVZPGRSLRLSCAASGFTF-SNYAMHWVRQPPGKGLEWVAVISYBGBBKY
                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY
                                                                                                                                                                                                                                                                       60 YABSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLYGBYRAFNYWGQG 115
                                                                                                                                                                                                                                        61 NP-SVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWH-FAVWGQG 114
                                                                3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686C11235.
Name-DKFZp686C11235;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG
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      DB 1; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
Query Match
63.2%; Score 393.5; DB 1; Length
Best Local Similarity 65.5%; Pred. No. 2.7e-32;
Matches 76; Conservative 15; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.0%; Score 392.5; DB 2; Length 70.4%; Pred. No. 3.3e-32; Live 10; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AA; 12843 MW; D0633949F2AC149D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, Immunol. Immunopathol. 87:184-192(1998).
EMBL, AR015023, AAD56259.1; -.
PIR, PH0875; PH0875.
PIR, S21205; S21205.
PIR, S30531; S30531.
HSSP, P01793; JIGC.
INTERPO: JPR007110; JG-like.
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PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81; Conservative
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                              IGHM protein.
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                          20 BIQLVESGGGLVQPGGSLRLSCAASGFTFSS-FEMNWVRQAPGKGLEWLSYITRSGNTVY 78
                                                                                                                                                                                                                                                                                  60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWH---FAVWGQG 114
                                                                                                                                                                                                                                                                                            Gaps
                                        The German Human cDNA Consortium;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                2,
                                                                                                                                                                                                              Query Match 62.8%; Score 391.5; DB 2; Length 473; Best Local Similarity 64.4%; Pred. No. 1.9e-31; Matches 76; Conservative 17; Mismatches 20; Indels 5.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                    PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS02290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 473 AA; 52121 MW; 9476EAE4COBFC447 CRC64;
                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                HSSP; P01861; 1ADQ.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig-1ike.
InterPro; IPR003597; Ig-1i.
InterPro; IPR003596; Ig-MC.
InterPro; IPR003596; Ig-V.
Ffam; PP07654; C1-set; 3.
SMART; SM00409; IG:2; SMART; SM00407; IGC1; 3.
                                                                         EMBL; BX640853; CAE45920.1; -
                                intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                       SEQUENCE FROM N.A.
TISSUE=Human small
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
        NCBI_TaxID=9606;
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Q6GMY2
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TISSUB-Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUSPERG R.L., Feingold B.A., Grouse L.H., Derge J.G.,

MI Klausner R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Mhiting M., Madan J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

M. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSH-----YFGHW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLVESGGGGLVKPGGSLRLSCAASGFTF-SDYYMSWIRQAPGKGLEWVSYISSSSSYTN 78
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 606;
TISSUE=Primary B-Cells;
SEQUENCE FROM N.A.
SIGNALSHORE R.;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073758; AAH73758.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003599; Ig_cl.
R InterPro; IPR003596; Ig_W.C.
R InterPro; IPR003596; Ig_W.C.
R Pfam; PF00047; Ig. 4.
R SWART; SW00409; IG; 2.
R SWART; SW00409; IG; 2.
R SWART; SW00406; IGV; 1.
R PROSITE; PS50835; IG_LIKE; 5.
R PROSITE; PS50835; IG_LIKE; 5.
R PROSITE; PS50835; IG_MHC; UNKNOWN_3.
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.5e-31;
.es 20; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 62.8%; Score 391.5; Local Similarity 62.5%; Pred. No. 2.5e es 80; Conservative 13; Mismatches
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYS-GETK 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCA---RGSHYFGHW-HFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE=Human esophagua tumor;
The German Human cDNA Consortium;
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiene (Human).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                  | Tisbub=rines, | Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. | EMBL; BC01576; AAH15760.1; -. | PRBL; S05271; S05271. | S05271; S05271. | Tisbub=rines | PRSP; P01861; 1ADQ. | RISP; P01861; 1ADQ. | RINE-Pro; IPR00710; Ig_c1. | RINE-Pro; IPR003597; Ig_c1. | RINE-Pro; IPR003597; Ig_c1. | RINE-Pro; IPR003596; Ig_V. | Rine-Pro; IPR00466; IGV; I. | SMART; SW00406; IGV; I. | DR PROSITE; PS50835; IG_LIKE; 5. | DR PROSITE; PS00290; IG_MHC; UNRNOWN 3. | SEQUENCE 597 AA; 65039 MM; 4PCA3ADBECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.8%; Score 391; DB 2; Length 597; 68.9%; Pred. No. 2.8e-31; Arive 12; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640947; CAE45972.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKF2p686G11190.
Name-DKFZp686G11190;
und mouse cDNA sequences.";
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00409; IG; 2.
SMART; SM00407; IGcl; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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InterPro; IPR0031599; IG.
InterPro; IPR003109; IG-like.
InterPro; IPR003597; IG_CI.
InterPro; IPR0031006; IG_MHC.
InterPro; IPR003596; IG_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 68.9%
Matches 82; Conservative
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                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Han M., Wiemann S. Submitted (AUG-200
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Q6MZQ6
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Gaps

Conservative

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79 YADSVKGRFTISGDISTNTLYLQMHSLRADDTAVYYCARADYRDYQVSPAYWYFDVWGRG 138
                                                                                                                  60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYF-----GHWHFAVWGOG 114
1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG-ETK 59
                               20 EVQLIESGGGIVQPGGSLRLSCAASGFTFRN-YAMNWVRQAPGKGLEWVSGISSSGVNTY 78
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Search completed: June 3, 2005, 09:16:14 Job time: 33.7497 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 3, 2005, 08:53:28; Search time 7.09576 Seconds (without alignments) 1545.812 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-791-619-12 625 1 EVQLVESGGGLVQPGGSLRL......YCARGSHYFGHWHFAVWGQG 114

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	q heavy chain	g heavy chain	0		ы	ы	g heavy chain -	g heavy	б	ы		ס	g heavy chain V	g heavy chain V	heavy chain -	heavy	chain V	heavy	heavy chain -	Ig heavy chain V r	heavy chain V	heavy	Ig heavy chain - h	heavy	heavy chain V	heavy chain -		heavy cha	Ig heavy chain pre
SUMMARIES		7044	S31588	S31114	S31666	E36005	S48797	831113	S31117	S31669	137780	S19666	G36005	S36259	S30531	S31107	S31701	S31598	S31686	S38489	S31603	S26794	831601	831116	S31674	S46390	831108	F36005	3167	S05271
	138								~									7												
	Length	~	140	123	138	122	128	121	122	141	147	121	121	117	125	119	137	135	140	127	132	123	130	118	139	114	119	119	134	160
	Query Match			67.0	66.7		Ġ.		65.7	55.7	55.7	9.59	9.59	55.4	55.4	65.3	65.2	65.0	54.8			•	•	64.2	64.2	54.1	64.0	64.0	64.0	54.0
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	Score	18	420	419	417	LO.	415.5	414	۲.	410.5	410.5	410	410	409	409	408	407.5	406	405	404	403	402	0	401.5	401.5	400.5	400	400	400	400
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Ig heavy chain - h	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	anti-tetanus toxin	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain - h	Ig heavy chain (su	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain - h
10	82	35	86	24	80	37	80	0	80	2	3	4	0	1	33
831110	S207	D360	PL0098	823624	8362	83158	PC239	S3627	S4879	C3600	15567	83110	83169	S46391	S38493
2 8311	2 S207	2 D360	2 PL00	2 \$236	2 \$362	2 83158	2 PC239	2 \$3627	2 \$4879	2 C3600	2 I5567	2 83110	2 83169	2 \$4639	2 83849
116 2 8311	2	0	~	~	0	7	7	7	7	7	7	0	7	N	7
010	124 2	119 2	130 2	143 2 (114 2	136 2	122 2	117 2	120 2	119 2	121 2	121 2	134 2	114 2	123 2
116 2	63.9 124 2	63.8 119 2	63.8 130 2	63.8 143 2 8	63.8 114 2	63.8 136 2	63.6 122 2	117 2	63.4 120 2	63.4 119 2	63.4 121 2	63.4 121 2	63.4 134 2	63.3 114 2	123 2

ALIGNMENTS

5 5 4 7 5 8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Similarity 73.0%; Fred. No. 6.1e-30; 4; Conservative 8; Mismatches 20; EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQ;
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RESULT 2
831588
Ig heavy chain V region - human (fragment)
C;Species Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 831588
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A;Reference number: 831588
A;Reference number: 831588
A;Reference number: 831588
A;Reference number: MALA
A;Reference number: MALA
A;Residues: 1-140 <cUI>A;Cross-references: EMBL: 214200; NID:930957; PIDN:CAA78569.1; PID:930958
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Length 140; Score 420; DB 2; Pred. No. 6.7e-30; 67.2%; 71.3%; Query Match Best Local Similarity

```
C,Accession: E36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-128 <a href="Mailto:AMJ">A; Rosid:A; Mailto:A; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13.Jan-1995 #sequence_revision 13.Sep-1998 #text_change 23.Jul-1999
C;Accession: S48797; S26893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSS-YGMHWVRQAPGKGLEWVAVIWYDGSNKY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTN- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSS-YAMHWVRQAPGKGLEWVAVISYDGSNKY 59
                                                                                                                                                                                                Ig heavy chain V region (M72) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRH-SSSWYYGMDVWGQG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFA--VWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTN-
79 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAR--TGYWYFDLWGRG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-98 - TOM>
A; Cross-references: BMBL: Z12350; NID: 932922; PIDN: CAA78220.1; PID: 932923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: GDB:IGH0; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.5%; Score 415.5; DB 2; Length Best Local Similarity 70.9%; Pred. No. 1.4e-29; Matches 83; Conservative 12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:M34030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S48797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-122 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: E36005
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Matches
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31666
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Pougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991 C;Superfamily: immunoglobilin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSS-YAMSWVRQAPGKGLEWVSAISGSGGSTY
                                                                               EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIT-YDGSTN
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2; Gaps
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                                                                                                                                                                                                                                                                                    YADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKDHDYSNYIYFDYWGGG 133
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                                                                                                                                                                                                                                      60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
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l Similarity 70.4%; Pred. No. 1.2e-29; 
81; Conservative 16; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 123;
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18; Indels
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Pred. No. 7.2e-30;
13; Mismatches
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71.8%;
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Conservative
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Best Local Similarity
Matches 84; Conserv
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Best Local Similarity
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A;Residues: 1-123 <RAA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S31114
Ig heavy chain - human
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82;
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Length 128;

Indels

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Sil669
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: Sil669
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the & A;Reference number: Sil585
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C;Species: Homo sapiens (man)
C;Date: 16-Peb-1996 #sequence_revision 16-Peb-1996 #text_change 23-Jul-1999
C;Accession. 137780; 255474
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by ht. A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: 137780
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Ig heavy chain V region (VH3DJH4) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19666
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
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A;Molecule type: mRNA
A;Residues: 1-141 <CUI>
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A;Molecule type: mRNA
A;Residues: 1-147 <RES>
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Best Local S:
Matches 82
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CiSpecies: Homo sapiens (man)
CiDate: 0.2-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
CiAccession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman R;Raaphorst, F.M.; Timminol. 22, 247-221, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A; Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: S31113
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
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A;Residues: 1-122 <RAA>
A;Cross-references: EMBL:X62967
A;Notes: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                               60 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDNYYYDSSGYYYYYYGMDVWG 119
YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYF---GHWHF----AVWG 112
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A,Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision.26-May-1995 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATDWGFYGRSAFDIWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 414; DB 2;
; Pred. No. 1.9e-29;
14; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4e-29;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.7%; Score 410.5; 71.6%; Pred. No. 4e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.2%;
70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: X62962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81; Conservative
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Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Residues: 1-121 <RAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                          Ig heavy chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                   8 114
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A;Status: preliminar
   9
                                                                                                                   113
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Best Local
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A,Gross-references: EMBL:X62955
A,Ross-references: EMBL:X62955
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 YADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARSRNYDSSGYYSH-YFDYWGGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCAR-----GSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTN- 59
                                                                                                                                                                                                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YGMFHWVLQAPGKGLEWVAFIRYDGSNKY 59
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                                                                                                                                                                                                                                                                                                                                                                                    60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFG----HWHFAVWGQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                  60 YADSVKGRFTISRDNSKATLYLQMNSLRAEDTAVYYCVREDHVITTGRYHYYMDVWGK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S30531
R;Marlette, X.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YSMNWVRQAPGKGLEWISYISSSSTIY
                                                                                                                                                                                                          Gaps
A, Cross-references: EMBL:218850; NID:g33123; PIDN:CAA79302.1; PID:g939902 C. Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin P:15-98/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                 Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9UL91; EMBL:Z18317
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 125
                                                                                                                                                                                                          21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.4%; Score 409; DB 2; Best Local Similarity 69.2%; Pred. No. 5.5e-29; Matches 83; Conservative 12; Mismatches 17;
                                                                                                                                                 Score 409; DB 2;
Pred. No. 5.1e-29;
                                                                                                                                  65.4%; Score 69.5%; Pred. No. 5.1e-2.
                                                                                                                                              Query Match
Best Local Similarity 69.5*
Matches 82; Conservative
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-125 < MAR>
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S30531
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C.Species: 103-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C.Accession: S36259
R.Gariffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A.Fitle: Human anti-self antibodies with high specificity from phage display libraries.
A.Reference number: S36256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. US.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on A;Reference number: $19663; MUID:92085276; PMID:1748994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSS-YGMHWYRQAPGKGLEWVAVISYDGSNKY
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                                                                                                                                              A;Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1335369 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                         2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
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                                                                                                                                                                                                                                                                                               Length 121;
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: hereroteramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                      20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.6%; Score 410; DB 2; ilarity 71.3%; Pred. No. 4.3e-29; Conservative 11; Mismatches 20;
                                                                                                                                                                                                                                                                                               65.6%; Score 410; DB 2; 69.6%; Pred. No. 4.3e-29;
                                                                                                                                                                                                                                                                                            Query Match 65.6%; Score 410; DB Best Local Similarity 69.6%; Pred. No. 4.3e-Matches 80; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: Q8WUK1; GB:M34031
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A;Gene: GDB:IGH@; IGHDY1
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Best Local Similarity
Matches 82; Conserv
                                                      A, Accession: S19666
A, Molecule type: mRNA
A, Residues: 1-121 < MAR>
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A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
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⁻FDYWGQG 112 60 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDPGASYY-

Search completed: June 3, 2005, 09:17:51 Job time: 8.09576 secs

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Fri Jun 3 09:56:26 2005
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 3, 2005, 08:31:37; Search time 32.7497 Seconds (without alignments) 1782.523 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-791-619-12 625 1 BVQLVBSGGGLVQPGGSLRL.....YCARGSHYFGHWHFAVWGQG 114

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	homo sapien	homo sapien	homo	homo	homo	homod	homo	homo sapien	homo	homo	homo	homo	homod	homo	homo	homo sapien	homo	homo	homo	พน ย ท	caras	homo sapien	homo	homo	homo	homo	homo sapien	mus m	homo	homo	homo
	Descri	Q6pja4	Q9u190	Q9u172	Q8wuk1	Q9u171	Q65zc9	Q6in78	Q6gmy2	Q6pi81	Q9u193	Q6n089	Q6mzv7	Q9u191	P01768	Q9y509	Q6gmx2	5qq960	P01766	9nzm9Ö	P01793	P19181	06mzd6	Q8wu38	Q8nc16	Q8n5k4	Q9hcc1	P01764	Q99m22	Q96k68	P01767	P01771
SOUTHWINES	ID	Q6PJA4	Q9UL90	Q9UL72	QBWUK1	Q9UL71	Q652C9	Q61N78	Q6GMY2	Q6P181	Q9UL93	Q6N089	Q6MZV7	Q9UL91	HV3G_HUMAN	Q9Y509	Q6GMX2	Q96BB9	HV3E HUMAN	Q6MZŪ6	HV24 MOUSE	HV05_CARAU	Q6MZQ6	Q8WU38	QBNCL6	Q8N5K4	Q9HCC1	HV3C_HUMAN	Q99M <u>2</u> 2	Q96K68	HV3F_HUMAN	HV3J HUMAN
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	ength	470	113	118	613	121	240	466	909	478	116	472	473	118	122	147	493	597	120	464	123	116	475	573	493	499	112	117	479	494	115	121
ф	Query Match Length	65.9	65.6	64.6	64.1	64.0	64.0	64.0	63.8	63.5	63.2	63.2	63.1	63.0	62.8	62.8	62.7	62.7	62.6	62.6	62.4	62.0	62.0	62.0	61.4	61.4	61.4	61.3	9.09	9.09	0.09	60.0
	Score	412	410	403.5	400.5	400	400	400	398.5	397	395	395	394.5	393.5	392.5	392.5	σ	392	391	391	390	387.5	387.5	387.5	384	384	383.5	383	379	378.5	375	375
	Result No.	1	7	٣	4	2	ė	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

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374.5 374.5 373.5 372.3 371.5 370 369.5 368.5 367.5	367.5
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## ALIGNMENTS

RESULT 1

DR EMBL; BC018747; AAH18747.1; DR HSSP; PO1661; IADO. DR InterPro; IPR001599; Ig. DR InterPro; IPR0013597; Ig. DR InterPro; IPR003006; Ig. DR InterPro; IPR003006; Ig. DR InterPro; IPR003006; Ig. DR Pfam; PF07654; C1-set; 3. DR SWART; SW00409; IG; 2. DR SWART; SW00409; IG; 2. DR SWART; SW00406; IGv; 1. DR PROSITE; PS50835; IG LIKE; 4.
HSSP; POG InterPro InterPro InterPro InterPro InterPro Pfan; S SMART; SN SMART; SN SMART; SN SMART; SN SMART; SN
HSSP; POI InterPro InterPro InterPro InterPro InterPro Pfam; Pro SMART; SN SMART; SN SMART; SN SMART; SN
InterPro InterPro InterPro Pfam; Pro SMART; SN SMART; SN SMART; SN SMART; SN SMART; SN
Incertory Pfam; PF( SMART; SN SMART; SN SMART; SN PROSITE;
SMARI; SE SMARI; SP PROSITE;

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TISSUE=Primary B-Cells;
Strausberg R.;
                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGHM protein.
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                                                                                   etus.";
                                                                                                                                                                                                                                        Query Match
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                                                                                              20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSS-YWMSWVRQAPGKGLEWYANIKQDGSEKY
                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY
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                                                                                                                                  61 N-PSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCAR-GSHYFGHWHFAVWGQG 114
                                                                                                                                              79 YVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWYRDW-FDPWGQG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.6%; Score 410; DB 2; Length 113;
71.3%; Pred. No. 3.2e-33;
Live 9; Mismatches 14; Indels 10; Gaps
                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                   65.9%; Score 412; DB 2; Length 470; 72.4%; Pred. No. 9.5e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                           17; Indels
Hypothetical protein.
SEQUENCE 470 AA; 51715 MW; 7B49556AllFD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
PIME. AF035024; AAD56260.1; -.
PIME. S78486; S78486.
HSSP; P01772; ZFB4.
InterPro: IPR007110; Ig-like.
InterPro: IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                         11; Mismatches
                                                                                                                                                                                                                  113 AA.
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                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                PRT;
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                                             Best Local Similarity 72.48
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                             Young D.C.;
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Matches
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TISSUB-Primary B-Cells;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MELANDER R.D., Foligoid B.A., Grouse L.H., Derge J.G.,

MISCHALL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marueina K., Farmer A.A., Rubin G.M., Hong L.,

Marchard S., Loquellano M.F., Casavant T.L., Scheetz T.E.,

Mena S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Michards S., Worley K.C., Hale S., Garcia A.M., Gab R.A.,

Millalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Millalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milling M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,

Markesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Milling M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.;

Mannara M.A.;

Man
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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Pred. No. 1.5e-32;
9; Mismatches 17; Indels 5
SEQUENCE FROM N.A. MEDINE-9814934; DOI=10.1006/clin.1998.4531; MEDINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wun X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                               Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035042; AAD56278.1; -.
PIR; S21205; S21205.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; P50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Conservative
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1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTN- 59
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TISSUB-Peripheral Nervous System;

TISSUB-Peripheral Nervous System;

MEDLINE-22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.0%; Score 400; DB 2; Length 240;
69.2%; Pred. No. 7.2e-32;
ive 12; Mismatches 14; Indels 10; Gaps
                                 60 YADSVKGRPTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKVTTIYDRFDIWGQG 114
60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kontermann R.E., Wing M.G., Winter G.;
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
EMBL, Y13056, CAA73499.1; -.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007596; Ig-v.
Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv. 2.
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                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Last annotation update)
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05-JUL_2004 (TrEMBLrel, 27, Last seq
05-JUL_2004 (TrEMBLrel, 27, Last ann
                                                                                                                                                                                                           PRT;
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STRAIN=C1g/7;
MEDLINE=97362799; PubMed=9219263;
                                                                                                                                                                                                                                                                                                                                                            Single-chain Fv (Fragment).
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SEQUENCE
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                                                                                                                                             RESULT 6
Q652C9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK-----DWSEGVETFDIWGQG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSS-YGMHWVRQAPGKGLEWVAVISYDGSNKY
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.1%; Score 400.5; DB 2; Length 613; 67.5%; Pred. No. 1.8e-31; ative 11; Mismatches 15; Indels 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.0%; Score 400; DB 2; Length 121; 68.7%; Pred. No. 3.4e-32; Arive 14; Mismatches 20; Indels
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020240; AAH20240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG LIKE; S.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035643; AAD56279.1; -.
HSSP; P01852; INFD.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P01861; 1ADQ.
Pfam; PF07654; C1-set; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81; Conservative
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                                                                                                                                                                                                                                                                                                                                                      S31119; S31119.
S70442; S70442.
                                                                                G36005.
PH1642.
PH1643.
PH1645.
PH1646.
                                                                                                                                                                                                                                                                                           S15590.
S31116.
                                                                                                                                                                                                                                                                PL0120; PL0120
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Best Local Similarity
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                                                                                                                                          PH1643;
PH1645;
                                                                                                                     PH1642;
                                                                                                                                                                                                                                                                                                                             831116;
                                                                                                                                                                                                        PH1646;
                                                                                                                                                                                                                                                                                           $15590;
                                                                                   G36005;
                                                                                                                                                                                                                                 PL0098;
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci D., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McKernan R.J., McKernan K.J., Malek, Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Banchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 EVQLVESGGGLIQPGGSLTLSCAASGLTVSSNY-MHWVRQAPGKGLEWVSVLYIGGATYY
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TISSUE=Primary B-Cells,

MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, BC072419, AAH7419-1; -... BMBL, BC072419, Ig-1; -... InterPro; IPR003199; Ig-1; -... InterPro; IPR003199; Ig-2, IRCAPT, BW00409; Ig-4, SWART; SW00407; IGG; 2... SWART; SW00406; IGv; 1... SWART; SW00406; IGv; 1... SWART; SW00406; IGv; 1... SWART; SW00409; IG IKE; 4... BROSITE; PS00290; IG IKE; 4... BROSITE; PS00290; IG IKE; 4... SWART; SW00406; IGV; 1... REQUENCE 466 AA; 50853 MW; 53EBOBCEDEB1076E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg \bar{R}.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSH-------YFGHW 106
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Villalon D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A., Fahey J., Heltron E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                        Generation and initial analysis of more than 15,000 full-length human
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MEDLINE=21388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingeld E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

TISSUE=Primary B-Cells;
A Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; BC073758; AAH73758.1; -.
RITEPTO; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR003597; Ig.cl.
RITEPTO; IPR003597; Ig.cl.
RITEPTO; IPR003596; Ig.W.
RITEPTO; IPR003596; Ig.W.
RITEPTO; IPR003596; Ig.W.
REPTO; IPR003596; Ig.W.
REPTO; IPR00409; IG.2.
SWART; SW00409; IG.2.
SWART; SW00409; IG.1.
REPTO; IPR00309; IG.1.
SWART; SW00409; IG.1.
REPTO; IPR00309; IRR00309; IRR00309; IRR00309; IRR003099; IRR00309
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Pred. No. 2.8e-31;
Tarthes 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 606 AA; 66184 MW; B6B38B51114E4C55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 AA
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1 Similarity 63.3%; Pred. No. 2.8e
81; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA sequences."
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Best Local Similarity
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us-10-791-619-12.rup

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HSSP; P01772; 2FB4.
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Q6MZV7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 YVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTWTTVNADYY-YFYMDV 137
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Varyanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 BVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YMMSWVRQAPGKGLEWVANIKQDGSEKY
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16, Indels 12,
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                         Strausberingly Decile;
Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL; BCO41037; AAH41037.1; -.
R HSSP; PO1861; 1ADQ.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 3.
R SMART; SM00409; IG; 1.
R R SMART; SM00409; IG; 1.
R R PROSITE; PS00290; IG LIKE; 4.
R PROSITE; PS00290; IG LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5%; Score 397; DB 2; Length 478;
65.3%; Pred. No. 3.1e-31;
ive 15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
WAY-2000 (TrEMBLrel. 13, Last sequence update).
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypotherical protein.
SEQUENCE 478 AA; 52666 MM; 17BED38D917970D6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF035021; AAD56257.1; -. PIR; PH1644; PH0644. PIR; PL0120; PL0120.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                               IISSUE=Primary B-Cells;
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20911.93
AC 09011.93
AC 09011.93
DT 01-MA DT 01-MA DE 01-MA DE Myosi
DE (Frag OS Eukar OC Eukar OC Mamma OC Eukar OC Mamma OC MAMMA N. [1]
RA MEDII RA WU X. MEDII RA MYOS RT "MYOS RT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 BVQLVESGGGLVQPGRSLRLSCAASGFTF-DDYAMHWVRQAPGKGLEWVSGISWNSGSIA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VQLVESGGGVVQPGRSLRLSCAASGFTFSS-YAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                                                                  2 VOLVESGGGLVOPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTN-Y
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                                                                                                                                                                                                 6; Gaps
                                                                                                                                                                                                                                                                                                                                      60 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCAGG----GGLGLGYWGQG 109
                                                                                                                                                                                                                                                                                                                  61 NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                         Length 116;
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66.7%; Pred. No. 4.8e-31;
ive 16; Mismatches 19; Indels
                                                                                                                                                         Query Match 63.2%; Score 395; DB 2; Length 11 Best Local Similarity 70.2%; Pred. No. 1e-31; Matches 80; Conservative 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          il protein.
472 AA; 51724 MW; 26CB340D0046D279 CRC64;
                                                                                                                    0DA0348154DD6061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686P15220.
Name-DKFZp686P15220;
Phypocate (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Human rectum tumor;
The German Human cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-v.
SMATT; SM00406; IG-v; I-
PR0SITE; PS50835; IG_LIKE; 1.
NON TER 1 1 1
NON TER 116
SEQÜENCE 116 AA; 12434 MW;
                                                                                                                    116 AA; 12434 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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Hypothetical protein DKFzp686C11235 Name=DKFzp686C11235;

Homo sapiens (Human)

NCBI_TaxID=9606;

S WE WAY TO THE STANDARD OF TH

PRT;

PRELIMINARY;

CAZM9C

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1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGST-- 58
                                                                                                                                                                                                                                                                                         1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YSMNWVRQAPGKGLEWV---SYISSTII 56
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                                                                                                                                                                                                                                                                                                                                                    59 --NYNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                             57 TIYYADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARGD---SSEAFDIWGQG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVELVVESGGGVVZPGRSLRLSCAASGFTF-SNYAMHWVRQPPGKGLEWVAVISYBGBBKY
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                                                                                                                                                                                                                     11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lehman D.W., Putnam F.W.;
"Amino acid sequence of the variable region of a human mu chain:
"Amino acid sequence of the segment.";
Procation of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
-i- MISCELLANEOUS: This mu chain was isolated from the plasma of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
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                                                                                                                                                                          DB 2; Length 118;
                                                                                                                                                                        63.0%; Score 393.5; DB 2; Length 69.5%; Pred. No. 1.5e-31; ive 9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig-like.
Pyrrolidone carboxylic acid.
                                                                                        1
118 118
118 AA; 12843 MW; D0633949F2AC149D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 122
122 AA, 13668 MW, A42D0F17D252F1C2 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patient with macroglobulinemia.
--- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02021; M3HUAM.
HSSP; P01772; 2FB4.
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PRART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=81013859; PubMed=6774332;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig-v.
SMRRT; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                              Local Similarity 69.5
les 82, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 EIQLVESGGGLVQPGGSLRLSCAASGFTFSS-FEMIWVRQAPGKGLEWLSYITRSGNTVY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWH---PAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Gaps
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUE-Human small intestine;
The German Human cDNA Consortium;
Bloecker H., Boecher M., Wewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640853; CAE45920.1; -.
HSSP; P01861; 1ADQ.
                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
forus. "immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035023; AAD56259.1; -.
PIR; PH0875; PH0875.
PIR; 231055; S21205.
PIR; 330531; A30531.
HSSP; P01783; 11GC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.1%; Score 394.5; DB 2; Length 473; Best Local Similarity 64.4%; Pred. No. 5.4e-31; Matches 76; Conservative 18; Mismatches 19; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MW X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR00110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig-like.
InterPro; IPR003065; Ig-Mc.
InterPro; IPR003596; Ig-Mtc.
InterPro; IPR003596; Ig-Wt.
InterPro; IPR00409; IG, 2.
SWART; SW00400; IG; 2.
SWART; SW00406; IGv; 1.
PROSITE; PS00290; IG-MtC; UNKNOWN_2.
PROSITE; PS00290; IG-MtC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 473 AA; 52121 MW; 9476EAB4COBFC447 CRC64;
                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
  473 AA.
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PRELIMINARY;

09UL91 RESULT 13

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Homo sapiens (Human)

(Fragment)

NCBI_TaxID=9606;

ACC OCC OCT REA REA REA DE DE REA REA DE REA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 YAGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYYCAKDGNYFDSVGYYYAGIDYWGQG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
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                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.8%; Score 392.5; DB 2; Length 147; 65.0%; Pred. No. 2.4e-31; tive 15; Mismatches 20; Indels 7.
                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH3 protein (Fragment).
                                   147 AA
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 65.0%
Matches 78; Conservative
                                PRELIMINARY;
                                                                                                                                                                                                                                           Name=VH3;
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